SEQUENCE LISTING

(1) GENERAL INFORMATIO

5 (i) APPLICANT: Ashkenazi, Avi J.

Baker, Kevin

Chuntharapai, Anan

Gurney, Austin

Kim, Kyung Jin

Wood, William

- (ii) TITLE OF INVENTION: Apo-2DcR
- (iii) NUMBER OF SEQUENCES: 13
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Genentech, Inc.
 - (B) STREET: 1 DNA Way
 - (C) CITY: South San Francisco
 - (D) STATE: California
 - (E) COUNTRY: USA
 - (F) ZIP: 94080
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: WinPatin (Genentech)
- 30 (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE: 12-Jun-1998
 - (C) CLASSIFICATION:
- 35 (vii) PRIOR APPLICATION DATA:

	((C) R	EFER]	ENCE,	/DOC	KET I	NUMB	ER:	P111	0P1				
10	(ix) T	CELEC							:					
	((B) T	ELEF	AX: (650/	952-9	9881							
	(2) INFO				•									
	(i) S	SEQUE	NCE (CHAR	ACTE	RIST	ICS:							
1 5 △1		(A) L					acio	as						
		(B) T												
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15 15 20	(xi) S	SEQUE	NCE I	DESCI	RIPT	ION:	SEQ	ID I	NO:1	:				
	Met Ala	Arg	Ile	Pro	Lys	Thr	Leu	Lys	Phe	Val	Val	Val	Ile	Val
	1			5					10					15
[] [] [] []	Ala Val	Leu	Leu	Pro	Val	Leu	Ala	Tyr	Ser	Ala	Thr	Thr	Ala	Arg
2 5				20					25					30
·	Gln Glu	Glu	Val	Pro	Gln	Gln	Thr	Val	Ala	Pro	Gln	Gln	Gln	Arg
				35					40					45
30	His Ser	Phe	Lys	Gly	Glu	Glu	Cys	Pro	Ala	Gly	Ser	His	Arg	
				50					55					60
	Glu His	Thr	Gly	Ala	Cys	Asn	Pro	Cys	Thr	Glu	Gly	Val	Asp	
				65					70					75
35					,									

(A) APPLICATION NUMBER: 60/049911

(B) FILING DATE: 18-JUN-1997

(A) NAME: Marschang, Diane L.

(B) REGISTRATION NUMBER: 35,600

(viii) ATTORNEY/AGENT INFORMATION:

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-	(2)	INFORMATION	FOR	SEQ	TD	NO:2:

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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1180 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single

10

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GCTGTGGGAA CCTCTCCACG CGCACGAACT CAGCCAACGA TTTCTGATAG 50

ATTTTTGGGA GTTTGACCAG AGATGCAAGG GGTGAAGGAG CGCTTCCTAC 100

CGTTAGGGAA CTCTGGGGAC AGAGCGCCCC GGCCGCCTGA TGGCCGAGGC 150

AGGGTGCGAC CCAGGACCCA GGACGGCGTC GGGAACCATA CC ATG 195

Met

1

GCC CGG ATC CCC AAG ACC CTA AAG TTC GTC GTC GTC ATC 234 Ala Arg Ile Pro Lys Thr Leu Lys Phe Val Val Ile

> 10 5

GTC GCG GTC CTG CCA GTC CTA GCT TAC TCT GCC ACC 273 Val Ala Val Leu Leu Pro Val Leu Ala Tyr Ser Ala Thr

15 20 25

ACT GCC CGG CAG GAG GAA GTT CCC CAG CAG ACA GTG GCC 312

Thr Ala Arg Gln Glu Glu Val Pro Gln Gln Thr Val Ala

					45					50				
5	CCA	GCA	GGA	TCT	CAT	AGA	TCA	GAA	CAT	ACT	GGA	GCC	TGT	390
	Pro	Ala	Gly	Ser	His	Arg	Ser	Glu	His	Thr	Gly	Ala	Cys	
		55					60					65		
	AAC	CCG	TGC	ACA	GAG	GGT	GTG	GAT	TAC	ACC	AAC	GCT	TCC	429
10	Asn	Pro	Cys	Thr	Glu	Gly	Val	Asp	Tyr	Thr	Asn	Ala	Ser	
				70					75					
	AAC	AAT	GAA	CCT	TCT	TGC	TTC	CCA	TGT	ACA	GTT	TGT	AAA	468
	Asn	Asn	Glu	Pro	Ser	Cys	Phe	Pro	Cys	Thr	Val	Cys	Lys	
1 5	80					85					90			
	TCA	GAT	CAA	AAA	CAT	AAA	AGT	TCC	TGC	ACC	ATG	ACC	AGA	507
	Ser	Asp	Gln	Lys	His	Lys	Ser	Ser	Cys	Thr	Met	Thr	Arg	
			95					100					105	
	GAC	ACA	GTG	TGT	CAG	TGT	AAA	GAA	GGC	ACC	TTC	CGG	AAT	546
	Asp	Thr	Val	Cys	Gln	Cys	Lys	Glu	Gly	Thr	Phe	Arg	Asn	
					110					115				
	GAA	AAC	TCC	CCA	GAG	ATG	TGC	CGG	AAG	TGT	AGC	AGG	TGC	585
	Glu	Asn	Ser	Pro	Glu	Met	Cys	Arg	Lys	Cys	Ser	Arg	Cys	
		120					125					130		
	CCT	AGT	GGG	GAA	GTC	CAA	GTC	AGT	AAT	TGT	ACG	TCC	TGG	624
30	Pro	Ser	Gly	Glu	Val	Gln	Val	Ser	Asn	Cys	Thr	Ser	Trp	
				135					140					
	GAT	GAT	ATC	CAG	TGT	GTT	GAA	GAA	TTT	GGT	GCC	AAT	GCC	663
	Asp	Asp	Ile	Gln	Cys	Val	Glu	Glu	Phe	Gly	Ala	Asn	Ala	
35	145					150					155			

CCA CAG CAA CAG AGG CAC AGC TTC AAG GGG GAG GAG TGT 351

Pro Gln Gln Arg His Ser Phe Lys Gly Glu Glu Cys

	ACT	GTG	GAA	ACC	CCA	GCT	GCT	GAA	GAG	ACA	ATG	AAC	ACC	702
	Thr	Val	Glu	Thr	Pro	Ala	Ala	Glu	Glu	Thr	Met	Asn/	Thr	
			160					165					170	
5	AGC	CCG	GGG	ACT	CCT	GCC	CCA	GCT	GCT	GAA	GAG	ACA	ATG	741
	Ser	Pro	Gly	Thr	Pro	Ala	Pro	Ala	Ala	Glu	Glu	Thr	Met	
					175					180				
	AAC	ACC	AGC	CCA	GGG	ACT	CCT	GCC	CCA	GCT	GCT	GAA	GAG	780
10	Asn	Thr	Ser	Pro	Gly	Thr	Pro	Ala	Pro	Ala	Ala	Glu	Glu	
		185					190					195		
	ACA	ATG	ACC	ACC	AGC	CCG	GGG	ACT	CCT	GCC	CCA	GCT	GCT	819
	Thr	Met	Thr	Thr	Ser	Pro	Gly	Thr	Pro	Ala	Pro	Ala	Ala	
#5 # 2				200					205					
	GAA	GAG	ACA	ATG	ACC	ACC	AGC	CCG	GGG	ACT	CCT	GCC	CCA	858
	Glu	Glu	Thr	Met	Thr	Thr	Ser	Pro	Gly	Thr	Pro	Ala	Pro	
	210					215					220			
	GCT	GCT	GAA	GAG	ACA	ATG	ACC	ACC	AGC	CCG	GGG	ACT	CCT	897
	Ala	Ala	Glu	Glu	Thr	Met	Thr	Thr	Ser	Pro	Gly	Thr	Pro	
			225					230					235	
<u>1</u> 25	GCC	TCT	TCT	CAT	TAC	CTC	TCA	TGC	ACC	ATC	GTA	GGG	ATC	936
	Ala	Ser	Ser	His	Tyr	Leu	Ser	Cys	Thr	Ile	Val	Gly	Ile	
					240					245				
	ATA	GTT	СТА	ATT	GTG	CTT	CTG	ATT	GTG	TTT	GTT	T 97	70	
30	Ile	Val	Leu	Ile	Val	Leu	Leu	Ile	Val	Phe	Val			
		250					255				259			
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AGGCGCTGGC TGAGGGCGGG GGGCGCTGGA CACTCTCTGC CCTGCCTCCC 1070

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TCTGCTGTGT TCCCACAGAC AGAAACGCCT GCCCCTGCCC CAAAAAAAA 1120

5 AAAAAAAA 1180

(2) INFORMATION FOR SEQ ID NO:3:

(i)	SPOUENCE	CHARACTERISTICS
$\lambda \perp I$	SECUENCE	CUMUNCIENTOITCO

(A) LENGTH: 299 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Gln Gly Val Lys Glu Arg Phe Leu Pro Leu Gly Asn Ser Gly
-40 -35 -30

Asp Arg Ala Pro Arg Pro Pro Asp Gly Arg Gly Arg Val Arg Pro -25

Arg Thr Gln Asp Gly Val Gly Asn His Thr Met Ala Arg Ile Pro
-10 -5 1 5

Lys Thr Leu Lys Phe Val Val Val Ile Val Ala Val Leu Leu Pro
10 20

Val Leu Ala Tyr Ser Ala Thr Thr Ala Arg Gln Glu Glu Val Pro
25 30

Gln Gln Thr Val Ala Pro Gln Gln Gln Arg His Ser Phe Lys Gly
40 45 50

Glu Glu Cys Pro Ala Gly Ser His Arg Ser Glu His Thr Gly Ala 60 65

	Cys	Asn	Pro	Cys	Thr 70	Glu	Gly	Val	Asp	Tyr 75	Thr	Asn	Ala	Ser	Asn 80
5	Asn	Glu	Pro	Ser	Cys 85	Phe	Pro	Cys	Thr	Val 90	Cys	Lys	Ser	Asp	Gln 95
	Lys	His	Lys	Ser	Ser 100	Cys	Thr	Met	Thr	Arg 105	Asp	Thr	Val	Cys	Gln 110
10	Cys	Lys	Glu	Gly	Thr 115	Phe	Arg	Asn	Glu	Asn 120	Ser	Pro	Glu	Met	Cys 125
	Arg	Lys	Cys	Ser	Arg 130	Cys	Pro	Ser	Gly	Glu 135	Val	Gln	Val	Ser	Asn 140
	Cys	Thr	Ser	Trp	Asp 145	Asp	Ile	Gln	Cys	Val 150	Glu	Glu	Phe	Gly	Ala 155
	Asn	Ala	Thr	Val	Glu 160	Thr	Pro	Ala	Ala	Glu 165	Glu	Thr	Met	Asn	Thr 170
	Ser	Pro	Gly	Thr	Pro 175	Ala	Pro	Ala	Ala	Glu 180	Glu	Thr	Met	Asn	Thr 185
25	Ser	Pro	Gly	Thr	Pro 190	Ala	Pro	Ala	Ala	Glu 195	Glu	Thr	Met	Thr	Thr 200
30	Ser	Pro	Gly	Thr	Pro 205	Ala	Pro	Ala	Ala	Glu 210	Glu	Thr	Met	Thr	Thr 215
	Ser	Pro	Gly	Thr	Pro 220	Ala	Pro	Ala	Ala	Glu 225	Glu	Thr	Met	Thr	Thr 230
35	Ser	Pro	Gly	Thr	Pro 235	Ala	Ser	Ser	His	Tyr 240	Leu	Ser	Cys	Thr	Ile 245

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	Val G	ly Ile	Ile	Val	Leu	Ile	Val	Leu	Leu	Ile	Val	Phe	
				250					255				259
	(2) IN	FORMATI	ON F	OR S	SEQ ]	ID NO	):4:						
5													
	(i)	SEQUEN					_						
		(A) LE						CS .					
		(B) TY											
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10		(D) IC	POLO	GI:	דיונ	car							
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	(122)		.02 2				~~ <u>~</u>						
<b>T</b> 5	GCTGT	GGGAA C	CCTCT	'CCAC	CG CC	GCACC	GAACT	r cac	GCCA/	ACGA	TTTC	CTGAT	TAG 50
	ATTTT'	TGGGA G	TTTG	ACCA	AG AC	3	ATG	CAA	GGG	GTG	AAG	GAG	90
							Met	Gln	Gly	Val	Lys	Glu	
							-40					-35	
<b>Ž</b> 0													
		TC CTA											129
	Arg P	he Leu			Gly	Asn	Ser	Gly	_	Arg	Ala	Pro	
				-30					-25				
<u>.</u> 1 1 2 5	aaa a		C A CD	aaa	CC A	aaa	7 00	ama.		aaa	7 00	7 00	1.00
25		CG CCT						_				_	168
•	_	ro Pro 20	Asp	СтУ	Arg	-15	Arg	Val	Arg	PIO	-10	1111	
		2 U				-15					- <b>T</b> O		
	CAG G	AC GGC	GTC	GGG	ልልሮ	САТ	ACC	АТС	GCC	CGG	ATC	CCC	207
30		sp Gly									_		

AAG ACC CTA AAG TTC GTC GTC GTC ATC GTC GCG GTC CTG 246 Lys Thr Leu Lys Phe Val Val Val Ile Val Ala Val Leu 10 15

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	Leu	Pro 20	Val	Leu	Ala	Tyr	Ser 25	Ala	Thr	Thr	Ala	Arg 30	Gln	
5	GAG	GAA	GTT	CCC	CAG	CAG	ACA	GTG	GCC	CCA	CAG	CAA	CAG	324
	Glu	Glu	Val	Pro 35	Gln	Gln	Thr	Val	Ala 40	Pro	Gln	Gln	Gln	
	AGG	CAC	AGC	TTC	AAG	GGG	GAG	GAG	TGT	CCA	GCA	GGA	TCT	363
10	Arg 45	His	Ser	Phe	Lys	Gly 50	Glu	Glu	Cys	Pro	Ala 55	Gly	Ser	
	CAT	AGA	TCA	GAA	CAT	ACT	GGA	GCC	TGT	AAC	CCG	TGC	ACA	402
	His	Arg	Ser 60	Glu	His	Thr	Gly	Ala 65	Cys	Asn	Pro	Cys	Thr 70	
i T	GAG	GGT	GTG	GAT	TAC	ACC	AAC	GCT	TCC	AAC	AAT	GAA	CCT	441
	Glu	Gly	Val	Asp	Tyr 75	Thr	Asn	Ala	Ser	Asn 80	Asn	Glu	Pro	
The control of the co	TCT	TGC	TTC	CCA	TGT	ACA	GTT	TGT	AAA	TCA	GAT	CAA	AAA	480
	Ser	Cys 85	Phe	Pro	Cys	Thr	Val 90	Cys	Lys	Ser	Asp	Gln 95	Lys	
<u>2</u> 5	CAT	AAA	AGT	TCC	TGC	ACC	ATG	ACC	AGA	GAC	ACA	GTG	TGT	519
	His	Lys	Ser	Ser 100	Cys	Thr	Met	Thr	Arg 105	Asp	Thr	Val	Cys	
	CAG	TGT	AAA	GAA	GGC	ACC	TTC	CGG	AAT	GAA	AAC	TCC	CCA	558
30	Gln	Cys	Lys	Glu	Gly	Thr	Phe	Arg	Asn	Glu	Asn	Ser	Pro	
	110					115					120			
	GAG	ATG	TGC	CGG	AAG	TGT	AGC	AGG	TGC	CCT	AGT	GGG	GAA	597
	Glu	Met	-	Arg	Lys	Cys	Ser		Cys	Pro	Ser	Gly		
35			125					130					135	

CTG CCA GTC CTA GCT TAC TCT GCC ACC ACT GCC CGG CAG 285

240

	Val	Gln	Val	Ser	Asn 140	Cys	Thr	Ser	Trp	Asp	Asp	Ile	Gln	
5	TGT	GTT	GAA	GAA	TTT	GGT	GCC	AAT	GCC	ACT	GTG	GAA	ACC	675
	Cys	Val	Glu	Glu	Phe	Gly	Ala	Asn	Ala	Thr	Val	Glu	Thr	
		150					155					160		
	CCA	GCT	GCT	GAA	GAG	ACA	ATG	AAC	ACC	AGC	CCG	GGG	ACT	714
10	Pro	Ala	Ala	Glu	Glu	Thr	Met	Asn	Thr	Ser	Pro	Gly	Thr	
				165					170					
	CCT	GCC	CCA	GCT	GCT	GAA	GAG	ACA	ATG	AAC	ACC	AGC	CCA	753
	Pro	Ala	Pro	Ala	Ala	Glu	Glu	Thr	Met	Asn	Thr	Ser	Pro	
	175					180					185			
	GGG	ACT	CCT	GCC	CCA	GCT	GCT	GAA	GAG	ACA	ATG	ACC	ACC	792
	Gly	Thr	Pro	Ala	Pro	Ala	Ala	Glu	Glu	Thr	Met	Thr	Thr	
<u> </u>	-		190					195					200	
	AGC	CCG	GGG	ACT	CCT	GCC	CCA	GCT	GCT	GAA	GAG	ACA	ATG	831
	Ser	Pro	Gly	Thr	Pro	Ala	Pro	Ala	Ala	Glu	Glu	Thr	Met	
			_		205					210				
<u>1</u> 25	ACC	ACC	AGC	CCG	GGG	ACT	CCT	GCC	CCA	GCT	GCT	GAA	GAG	870
	Thr	Thr	Ser	Pro	Gly	Thr	Pro	Ala	Pro	Ala	Ala	Glu	Glu	
		215					220					225		
	ACA	ATG	ACC	ACC	AGC	CCG	GGG	ACT	CCT	GCC	тст	TCT	CAT	909
30	Thr	Met	Thr	Thr	Ser	Pro	Gly	Thr	Pro	Ala	Ser	Ser	His	
				230					235					
	TAC	CTC	TCA	TGC	ACC	ATC	GTA	GGG	ATC	ATA	GTT	СТА	ATT	948

GTC CAA GTC AGT AAT TGT ACG TCC TGG GAT GAT ATC CAG 636

250

Tyr Leu Ser Cys Thr Ile Val Gly Ile Ile Val Leu Ile

GTG CTT CTG ATT GTG TTT GTT T GAAAGACTTC ACTGTGGAAG 990
Val Leu Leu Ile Val Phe Val
255 259

5 AAATTCCTTC CTTACCTGAA AGGTTCAGGT AGGCGCTGGC TGAGGGCGGG 1040
GGGCGCTGGA CACTCTCTGC CCTGCCTCCC TCTGCTGTGT TCCCACAGAC 1090
AGAAACGCCT GCCCCTGCCC CAAAAAAAAA AAAAAAAAA AAAAAAAAA 1140

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(i) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID NO:5:

- (A) LENGTH: 43 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

# TGTAAAACGA CGGCCAGTTA AATAGACCTG CAATTATTAA TCT 43

- (2) INFORMATION FOR SEQ ID NO:6:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 41 base pairs
    - (B) TYPE: Nucleic Acid
    - (C) STRANDEDNESS: Single
    - (D) TOPOLOGY: Linear
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

35

## CAGGAAACAG CTATGACCAC CTGCACACCT GCAAATCCAT T 41

(2) INFOR	MATION	FOR	SEQ	ID	NO: 7	<b>7</b> :
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1 -	١	CECTENCE	CHARACTERISTICS:
( )	- /	シログハロバイロ	CHARACIERISTICS

(A) LENGTH: 49 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His
1 10 15

Leu Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly
20 25 30

Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys
40
45

Gly Cys Arg Lys

49

# (2) INFORMATION FOR SEQ ID NO:8:

# (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr Thr Asn Ala Ser Asn
1 5 10 15

35

Asn Glu Pro Ser Cys Phe Pro Cys Thr Val Cys Lys Ser Asp Gln
20 25 30

Lys His Lys Ser Ser Cys Thr Met Thr Arg Asp Thr Val Cys Gln
35 40 45

Cys Lys Glu

48

- 10 (2) INFORMATION FOR SEQ ID NO:9:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 70 base pairs
    - (B) TYPE: Nucleic Acid
    - (C) STRANDEDNESS: Single
    - (D) TOPOLOGY: Linear
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGGAGCCGCT CATGAGGAAG TTGGGCCTCA TGGACAATGA GATAAAGGTG 50

GCTAAAGCTG AGGCAGCGGG 70

- (2) INFORMATION FOR SEQ ID NO:10:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1799 base pairs
    - (B) TYPE: Nucleic Acid
    - (C) STRANDEDNESS: Single
    - (D) TOPOLOGY: Linear
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

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	GCG	CCCA	CAA .	AATA(	CACC	GA C	GATG(	CCCG	A TC'	ract'	TTAA	GGG	CTGAZ	AAC 100
5	CCA	CGGG	CCT	GAGA	GACT	AT A	AGAG(	CGTT	C CC'	racc	GCC		GAA Glu	145
												1	Giu	
	CAA	CGG	GGA	CAG	AAC	GCC	CCG	GCC	GCT	TCG	GGG	GCC	CGG	184
10	Gln	Arg	Gly	Gln	Asn	Ala	Pro	Ala	Ala	Ser	Gly	Ala	Arg	
			5					10					15	
	AAA	AGG	CAC	GGC	CCA	GGA	CCC	AGG	GAG	GCG	CGG	GGA	GCC	223
A Company of the Comp	Lys	Arg	His	Gly	Pro	Gly	Pro	Arg	Glu	Ala	Arg	Gly	Ala	
					20					25				
Formula in the second s	AGG	ССТ	GGG	CTC	CGG	GTC	CCC	AAG	ACC	CTT	GTG	CTC	GTT	262
2	Arg	Pro	Gly	Leu	Arg	Val	Pro	Lys	Thr	Leu	Val	Leu	Val	
		30					35					40		
	GTC	GCC	GCG	GTC	CTG	CTG	TTG	GTC	TCA	GCT	GAG	TCT	GCT	301
Fr. T. S. S	Val	Ala	Ala	Val	Leu	Leu	Leu	Val	Ser	Ala	Glu	Ser	Ala	
				45					50					
<u>2</u> 5	CTG	ATC	ACC	CAA	CAA	GAC	CTA	GCT	CCC	CAG	CAG	AGA	GCG	340
	Leu	Ile	Thr	Gln	Gln	Asp	Leu	Ala	Pro	Gln	Gln	Arg	Ala	
	55					60					65			
	GCC	CCA	CAA	CAA	AAG	AGG	TCC	AGC	CCC	TCA	GAG	GGA	TTG	379
30	Ala	Pro	Gln	Gln	Lys	Arg	Ser	Ser	Pro	Ser	Glu	Gly	Leu	
			70					75					80	
	TGT	CCA	CCT	GGA	CAC	CAT	ATC	TCA	GAA	GAC	GGT	AGA	GAT	418
	Cys	Pro	Pro	Gly	His	His	Ile	Ser	Glu	Asp	Gly	Arg	Asp	
35					85					90				

CCCACGCGTC CGCATAAATC AGCACGCGGC CGGAGAACCC CGCAATCTCT 50

	100		100	+00			0 011	<b>V11V</b>	0110		1100	1101	0110	
	Cys	Ile	Ser	Cys	Lys	Tyr	Gly	Gln	Asp	Tyr	Ser	Thr	His	
		95					100					105		
5	TGG	AAT	GAC	CTC	CTT	TTC	TGC	TTG	CGC	TGC	ACC	AGG	TGT	496
	Trp	Asn	Asp	Leu	Leu	Phe	Cys	Leu	Arg	Cys	Thr	Arg	Cys	
				110					115					
	GAT	TCA	GGT	GAA	GTG	GAG	CTA	AGT	CCC	TGC	ACC	ACG	ACC	535
10	Asp	Ser	Gly	Glu	Val	Glu	Leu	Ser	Pro	Cys	Thr	Thr	Thr	
	120					125					130			
	AGA	AAC	ACA	GTG	TGT	CAG	TGC	GAA	GAA	GGC	ACC	TTC	CGG	574
- Annales - Control of the Control o	Arg	Asn	Thr	Val	Cys	Gln	Cys	Glu	Glu	Gly	Thr	Phe	Arg	
<b>1</b> 5			135					140					145	
Face the court  - American man  - American man														
	GAA	GAA	GAT	TCT	CCT	GAG	ATG	TGC	CGG	AAG	TGC	CGC	ACA	613
	Glu	Glu	Asp	Ser	Pro	Glu	Met	Cys	Arg	Lys	Cys	Arg	Thr	
permitten in a committen in a commit			<del></del>		150			_	_	155	_			
<u></u>														
	GGG	TGT	CCC	AGA	GGG	ATG	GTC	AAG	GTC	GGT	GAT	TGT	ACA	652
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Gly	Cys	Pro	Arg	Gly	Met	Val	Lys	Val	Gly	Asp	Cys	Thr	
		160					165					170		
<u>4</u> 25	CCC	TGG	AGT	GAC	ATC	GAA	TGT	GTC	CAC	AAA	GAA	TCA	GGC	691
	Pro	Trp	Ser	Asp	Ile	Glu	Cys	Val	His	Lys	Glu	Ser	Gly	
		•		175			•		180	•			•	
	ATC	ATC	ATA	GGA	GTC	ACA	GTT	GCA	GCC	GTA	GTC	TTG	ATT	730
30	Ile	Ile	Ile	Gly	Val	Thr	Val	Ala	Ala	Val	Val	Leu	Ile	
	185			_		190					195			
	GTG	GCT	GTG	TTT	GTT	TGC	AAG	TCT	TTA	CTG	TGG	AAG	AAA	769
	Val	Ala	Val	Phe	Val	Cys	Lys	Ser	Leu	Leu	Trp	Lys	Lys	
35			200			•	•	205			-	-	210	

TGC ATC TCC TGC AAA TAT GGA CAG GAC TAT AGC ACT CAC 457

	Val	Leu	Pro	Tyr	Leu 215	Lys	Gly	Ile	Cys	Ser 220	Gly	Gly	Gly	
5			CCT Pro											847
10			GAG Glu											886
			CCC Pro											925
			CCA Pro 265											964
25			GAG Glu											1003
25	_		TCT Ser	_						_		_		1042
30			GAT Asp											1081
35			GCA Ala											1120

GTC CTT CCT TAC CTG AAA GGC ATC TGC TCA GGT GGT 808

	CTC	ATG	AGG	AAG	TTG	GGC	CTC	ATG	GAC	AAT	GAG	ATA	AAG	1159
	Leu	Met	Arg	Lys	Leu	Gly	Leu	Met	Asp	Asn	Glu	Ile	Lys	
			330					335					340	
5	ርሞር	ር ር ር	ΔΔΔ	ር ር ፓ	GAG	GCA	GCG	GGC	$C\Delta C$	AGG	GAC	ACC	ጥጥር	1198
J				Ala										1170
	vaı	AIA	пуъ	AIA	345	AIA	AIA	GIY	птэ	350	Asp	1111	пеа	
					242					330				
	TAC	ACG	ATG	CTG	ATA	AAG	TGG	GTC	AAC	AAA	ACC	GGG	CGA	1237
10	Tyr	Thr	Met	Leu	Ile	Lys	Trp	Val	Asn	Lys	Thr	Gly	Arg	
		355					360					365		
	GAT	GCC	тст	GTC	CAC	ACC	CTG	CTG	GAT	GCC	TTG	GAG	ACG	1276
				Val										
<u> </u>	- L			370					375					
	CTG	GGA	GAG	AGA	CTT	GCC	AAG	CAG	AAG	ATT	GAG	GAC	CAC	1315
	Leu	Gly	Glu	Arg	Leu	Ala	Lys	Gln	Lys	Ile	Glu	Asp	His	
The state of the s	380					385					390			
	TTG	TTG	AGC	TCT	GGA	AAG	TTC	ATG	TAT	CTA	GAA	GGT	AAT	1354
	Leu	Leu	Ser	Ser	Gly	Lys	Phe	Met	Tyr	Leu	Glu	Gly	Asn	
			395					400					405	
<u></u>	GCA	GAC	TCT	GCC	WTG	TCC	TAAC	TGTO	ATI	CTC	ГТСА	GGA	AGTG <i>I</i>	AGA 1400
	Ala	Asp	Ser	Ala	Xaa	Ser								
		_			410	411								
							- cm c c	~~ ~ ~ ~	3.00			~~ ~		<b>Y 7</b> 4 5 4
30	CCT"	rccc ₁	l'GG '.	I.I.I.Y(	:C:1"1"1	["I" 'I"]	.'C'I'GC	<del>S</del> AAAA	A AGC	CCAA	AC'I'G	GAC".	rccae	FTC 1450
	AGTA	AGGAI	AAG T	rgcc <i>r</i>	CAAI	T G1	CACA	ATGAC	C CGC	GTACT	rgga	AGA	ACTO	CTC 1500
	CC3.0	ቦረን ላ	\ <i>(</i> '')\	ריר <i>י</i> א ריר	ירא רח	ים כז	\ TPCC 7	\ <i>አ</i>	י פפח	נ עיה דיי	/ <b>С</b> плат	ውው <i>ር</i> ን	\ CPCC	CAC 1550
	CCAI	CCAF	ich l	) JRJ I	CAGI	.G GF	3 I GGF	ara Cra I		GIA	<i>7</i> (11	110	3C I G(	MC 133(

TTGGCATTAT TTTTATAAGC TGAATGTGAT AATAAGGACA CTATGGAAAT 1600

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GTCTGGATCA	TTCCGTTTGT	GCGTACTTTG	AGATTTGGTT	TGGGATGTCA	1650
TTGTTTTCAC	AGCACTTTTT	TATCCTAATG	TAAATGCTTT	ATTTATTAT	1700
TTGGGCTACA	TTGTAAGATC	CATCTACAAA	AAAAAAAAA	AAAAAAAAG	1750
GGCGGCCGCG	ACTCTAGAGT	CGACCTGCAG	AAGCTTGGCC	GCCATGGCC 1	799

(2) INFORMATION FOR SEQ ID NO:11:

10

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- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 411 amino acids
  - (B) TYPE: Amino Acid
  - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg
1 10 15

Lys Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro
20 25 30

Gly Leu Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val

40
45

Leu Leu Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp
50 55 60

Leu Ala Pro Gln Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser 70 75

Pro Ser Glu Gly Leu Cys Pro Pro Gly His His Ile Ser Glu Asp 80 85 90

35

	Gly	Arg	Asp	Cys	Ile 95	Ser	Cys	Lys	Tyr	Gly 100	Gln	Asp	Tyr	Ser	Thr 105
5	His	Trp	Asn	Asp	Leu 110	Leu	Phe	Cys	Leu	Arg 115	Cys	Thr	Arg	Cys	Asp 120
	Ser	Gly	Glu	Val	Glu 125	Leu	Ser	Pro	Cys	Thr 130	Thr	Thr	Arg	Asn	Thr 135
10	Val	Cys	Gln	Cys	Glu 140	Glu	Gly	Thr	Phe	Arg 145	Glu	Glu	Asp	Ser	Pro 150
<u>=</u> 1=5	Glu	Met	Cys	Arg	Lys 155	Cys	Arg	Thr	Gly	Cys 160	Pro	Arg	Gly	Met	Val 165
	Lys	Val	Gly	Asp	Cys 170	Thr	Pro	Trp	Ser	Asp 175	Ile	Glu	Cys	Val	His 180
	Lys	Glu	Ser	Gly	Ile 185	Ile	Ile	Gly	Val	Thr 190	Val	Ala	Ala	Val	Val 195
1 1 1 1 2 2 2 2 5	Leu	Ile	Val	Ala	Val 200	Phe	Val	Cys	Lys	Ser 205	Leu	Leu	Trp	Lys	Lys 210
<b>□</b> 25	Val	Leu	Pro	Tyr	Leu 215	Lys	Gly	Ile	Cys	Ser 220	Gly	Gly	Gly	Gly	Asp 225
30	Pro	Glu	Arg	Val	Asp 230	Arg	Ser	Ser	Gln	Arg 235	Pro	Gly	Ala	Glu	Asp 240
30	Asn	Val	Leu	Asn	Glu 245	Ile	Val	Ser	Ile	Leu 250	Gln	Pro	Thr	Gln	Val 255
35	Pro	Glu	Gln	Glu	Met 260	Glu	Val	Gln	Glu	Pro 265	Ala	Glu	Pro	Thr	Gly 270

	Val	Asn	Met	Leu	Ser 275	Pro	Gly	Glu	Ser	Glu 280	His	Leu	Leu	Glu	Pro 285
5	Ala	Glu	Ala	Glu	Arg 290	Ser	Gln	Arg	Arg	Arg 295	Leu	Leu	Val	Pro	Ala 300
	Asn	Glu	Gly	Asp	Pro 305	Thr	Glu	Thr	Leu	Arg 310	Gln	Cys	Phe	Asp	Asp 315
10	Phe	Ala	Asp	Leu	Val 320	Pro	Phe	Asp	Ser	Trp 325	Glu	Pro	Leu	Met	Arg 330
	Lys	Leu	Gly	Leu	Met 335	Asp	Asn	Glu	Ile	Lys 340	Val	Ala	Lys	Ala	Glu 345
	Ala	Ala	Gly	His	Arg 350	Asp	Thr	Leu	Tyr	Thr 355	Met	Leu	Ile	Lys	Trp 360
	Val	Asn	Lys	Thr	Gly 365	Arg	Asp	Ala	Ser	Val 370	His	Thr	Leu	Leu	Asp 375
	Ala	Leu	Glu	Thr	Leu 380	Gly	Glu	Arg	Leu	Ala 385	Lys	Gln	Lys	Ile	Glu 390
	Asp	His	Leu	Leu	Ser 395	Ser	Gly	Lys	Phe	Met 400	Tyr	Leu	Glu	Gly	Asn 405
3.0	Ala	Asp	Ser	Ala	Xaa 410										

- (2) INFORMATION FOR SEQ ID NO:12:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 29 base pairs
    - (B) TYPE: Nucleic Acid

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATCAGGGACT TTCCGCTGGG GACTTTCCG 29

(2) INFORMATION FOR SEQ ID NO:13:

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- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGGATGGGAA GTGTGTGATA TATCCTTGAT 30